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Matches 127; Conservative 26; Mismatches 58; Indels 4; Gaps 3;
 124 AGYKVISGGKSGSTTRYWDCCKASGWPVKASVTGPVDTCAISGILLDANAQGCC-N 182
 10 APLAVSAA-SGSGHSTFYWDCCKPSCSWGKAANAPALTCDKNDNPISNTNANGCEG 68
 183 GNGFMCMNPNFVAVNDELAYGFAAASGAGWCCGCGYELTFTTSGAASGKKVVQVVT 242
 69 GGSAYACTNYSFVAVNDELAYGFAATKISGSEASWCCACVALTFTTGPVKGMIVQST 128
 243 NTGGDLGSHHFDLPQGGGVIENGCAOMGAPNDGARYGVSSVSDCASLPSALQAG 302
 129 NTGGDLGSHHFDLPQGGGVIENGCAOMGAPNDGARYGVSSVSDCASLPSALQAG 186
 303 KQWRFNFKNSDNTMTFKEVTCPAELTTRSGCER 337
 187 CHWRFDWPNADNPDTFEQVQCPKALLDISGCKR 221

RESULT 2
 GUN5_HUMIN STANDARD; PRT; 213 AA.
 AC P43316;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Endoglucanase V (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
 DE (Cellulase V) (EG V).
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 OX NCBI_TaxID=34413;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Rasmussen G., Mikkelsen J.-M., Schulein M., Patkar S.A., Hagen P.,
 RA Hjort C.M., Hastrup S.;
 RA "A cellulase preparation comprising an endoglucanase enzyme";
 RA Patent number WO9117243, 14-NOV-1991.
 RL [2]
 RL X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RP MEDLINE=93390622; PubMed=8377830;
 RA Davies G.J., Dodson G.G., Hubbard R.E., Tolley S.P., Dauter Z.,
 RA Wilson K.S., Hjort C., Mikkelsen J.M., Rasmussen G., Schulein M.;
 RA "Structure and function of endoglucanase V";
 RL Nature 365:362-364 (1993).
 RN [3]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RP MEDLINE=96101453; PubMed=8519779;
 RA Davies G.J., Dodson G.G., Moore M.H., Tolley S.P., Dauter Z.,
 RA Wilson K.S., Rasmussen G., Schulein M.;
 RA "Structure determination and refinement of the Humicola insolens
 RT endoglucanase V at 1.5-A resolution";
 RL Acta Crystallogr. D 52:7-17 (1996).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
 CC HYDROLASES).
 DR PDB; 2ENG; 08-DEC-96.
 DR PDB; 3ENG; 16-JUN-97.
 DR PDB; 4ENG; 16-JUN-97.
 DR InterPro: IPR000334; GH 45.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS0140; GLYCOSYL_HYDROL_F45; 1.
 DR Cellulose degradation; Hydrolase; Glycosidase; 3D-structure.
 KW ACT_SITE 10 10 NUCLEOPHILE
 FT ACT_SITE 121 121 PHOTON DONOR
 FT SEQUENCE 213 AA; 22864 MW; 24334301BA3BC804 CRC64;
 SQ

Query Match 38.9%; Score 710; DB 1; Length 213;
 Best Local Similarity 62.1%; Pred. No. 1.7e-40; Indels 3;
 Matches 126; Conservative 25; Mismatches 46; Gaps 3;
 137 GSTTRYWDCCKASGWPVKASVTGPVDTCAISGILLDANAQGCCN-GNGFMCMNPNFV 195
 3 GRSTRYWDCCKPSCSWGKAANAPALTCDKNDNPISNTNANGCEG 62
 196 AVNDELAYGFAAASGAGWCCGCGYELTFTTSGAASGKKVVQVVTNTGGDLGSHHFDL 255
 63 AVNDELAYGFAAASGAGWCCGCGYELTFTTSGAASGKKVVQVVTNTGGDLGSHHFDL 122
 256 QMPGGGVIENGCAOMGAPNDGARYGVSSVSDCASLPSALQAGCKWRNFWFKNSD 314
 123 NIPGGGVIENGCAOMGAPNDGARYGVSSVSDCASLPSALQAGCKWRNFWFKNSD 178
 315 NPTMTFKEVTCPAELTTRSGCER 337
 179 NPSFSFRVQCPAELVARTGCKR 201
 RESULT 3
 GUNB_PSEFL STANDARD; PRT; 511 AA.
 AC P18126;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Endoglucanase B precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
 DE (Cellulase) (EGB).
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OX NCBI_TaxID=294;
 RN [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 30-48.
 RC STRAIN=Sp. Cellulosa;
 RE MEDLINE=90355836; PubMed=2117693;
 RA Gilbert H.J., Hall J., Hazlewood G.P., Ferreira L.M.A.;
 RA "The N-terminal region of an endoglucanase from Pseudomonas
 RT fluorescens subspecies cellulosa constitutes a cellulose-binding
 RL domain that is distinct from the catalytic centre";
 RL Mol. Microbiol. 4:759-767 (1990).
 CC -1- FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF 1,4-BETA-
 CC GLUCOSIDIC LINKAGES IN CELLULOSE, LICHENIN AND CEREAL BETA-D-
 CC GLUCANS. EGB IS MOST ACTIVE AGAINST BARLEY BETA-GLUCAN, BUT SHOWED
 CC SIGNIFICANT ACTIVITY AGAINST AMORPHOUS AND CRYSTALLINE CELLULOSE.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
 CC (CBD).
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
 CC HYDROLASES).
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 CC EMBL; X52615; CAA36844.1;
 CC PIR; S10527; S10527.
 CC HSP; P43316; 2ENG.
 DR InterPro: IPR001919; Bac celose-bind.
 DR InterPro: IPR002883; CBD_5.
 DR InterPro: IPR000334; GH_45.
 DR Pfam; PF00553; CBM_2; 1.
 DR Pfam; PF02013; CBM_10; 1.
 DR Pfam; PF02015; Glyco_hydro_45; 1.

[illegible]

DR PROSITE; PS00562; CBD FUNGAL; 1.
DR PROSITE; PS00655; GLYCOSYL HYDROL F6_1; 1.
DR PROSITE; PS00656; GLYCOSYL HYDROL F6_2; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 16
FT CHAIN 17 462
FT DOMAIN 17 65
FT DOMAIN 66 99
FT DOMAIN 100 462
FT ACT_SITE 190 190
FT ACT_SITE 236 236
FT ACT_SITE 416 416
FT ACT_SITE 33 50
FT DISULFID 44 60
FT DISULFID 191 250
FT DISULFID 383 430
FT CARBOHYD 37 37
FT CARBOHYD 223 223
FT CARBOHYD 272 272
FT CARBOHYD 317 317
SQ SEQUENCE 462 AA; 49207 MW; E25B2F5B828B637F CRC64;
Query Match 9.6%; Score 175.5; DB 1; Length 462;
Best Local Similarity 38.3%; Pred. No. 6.2e-05;
Matches 46; Conservative 13; Mismatches 42; Indels 19; Gaps 4;
QY 1 MKFTVAITSIAVALALSSAASCS-VYGGCGGIGWSGPTCCSGSTCVAQEGNKYYS 59
DB 1 MAYKLILAAFAATAALAAPEERQSCNSGQVWQCGQWNSGTPCCTSGNKC-V-KLNDFFYS 58
QY 60 QCLPGS--HSNNAGNASSTKTKSTTKATATVTTTKTATATVTTTKTSTTTAAAS 117
DB 59 QCQPGSAEPSTAGPSST-----TATKTTATGSSITAGGSVTSAPPAAS 104
RESULT 9
SIML YEAST STANDARD; PRT; 475 AA.
ID P40472; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SIM1 protein precursor.
GN SIM1 OR BP3 OR YIL123W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Cosey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Hornell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lye G., Moule S., Moulle T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skellton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP IDENTIFICATION.
RX MEDLINE=96155611; PubMed=8574583;
RA Dahmann C., Diffley J.F.X., Nasmyth K.A.;
RT "S-phase-promoting cyclin-dependent kinases prevent re-replication by
RT inhibiting the transition of replication origins to a pre-replicative
RT state".
RL Curr. Biol. 5:1257-1269(1995).
CC -!- FUNCTION: REQUIRED FOR THE MAINTENANCE OF THE CLBS KINASE
CC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE SUN FAMILY.
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FT DOMAIN 60 87
FT ACT_SITE 88 438
FT ACT_SITE 215 215
FT ACT_SITE 393 393
FT DISULFID 28 45
FT DISULFID 39 55
FT DISULFID 170 229
FT DISULFID 360 407
FT VARIANT 133 133
FT VARIANT 152 152
FT VARIANT 244 244
FT VARIANT 248 248
FT VARIANT 398 398
SQ SEQUENCE 438 AA; 46209 MW; 002C973544893794 CRC64;
Query Match 9.9%; Score 181; DB 1; Length 438;
Best Local Similarity 44.9%; Pred. No. 2.6e-05;
Matches 44; Conservative 13; Mismatches 27; Indels 14; Gaps 4;
QY 11 AVALALSSAE--AASCSVVGCGGIGWSGPTCCSGSTCVAQEGNKYYSQCLPGSHSN 68
DB 5 AALLALASLVPFVQAQSPVWQCGGNGTGTTCASGTCVKQ--NDFYSQCLP---NN 59
QY 69 NAGNASSTKTKSTTKTAKATATV-----TTKTV 99
DB 60 QAPPSTTQPTTPATTTSGGTGPTSGAGNPTGKT 97
RESULT 8
GUNB_FUSOX STANDARD; PRT; 462 AA.
ID P46236;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Putative endoglucanase type B precursor (EC 3.2.1.4) (Endo-1,4-beta-
DE glucanase) (Cellulase).
OS Fusarium oxysporum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5507;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95047531; PubMed=7959045;
RA Sheppard P.O., Grant F.J., Oort P.J., Sprecher C.A., Foster D.C.,
RA Hagen F.S., Upshall A., McKnight G.L., O'Hara P.J.;
RT "The use of conserved cellulase family-specific sequences to clone
RT cellulase homologue cDNAs from Fusarium oxysporum";
RL Gene 150:163-167(1994).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.
CC -!- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY B (FAMILY 6 OF GLYCOSYL
CC HYDROLASES).
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CC EMBL; L29377; AAA65585.1; -
DR HSSP; P07987; 1CB2.
DR InterPro; IPR000254; CBD fungal.
DR InterPro; IPR001524; GH 6.
DR Pfam; PF00734; CBM_1; 1.
DR PRINTS; PR001341; Glyco_hydro_6; 1.
DR PRODOM; PD001821; CBD_fungal; 1.
DR PRODOM; PD001821; CBD_fungal; 1.
DR SMART; SM00236; fCBD; 1.

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CC EMBL; U08843; AA61792.1; -.
DR HSP; P00725; 2CBH.
DR InterPro; IPR000254; CBD_fungal.
DR Pfam; PF00734; CBM_1; 4.
DR SMART; SM00236; fCBD; 4.
DR PROSITE; PS00562; CBD_FUNGAL; 4.
DR Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 210
FT DOMAIN 23 62
FT DOMAIN 63 105
FT DOMAIN 125 165
FT DOMAIN 166 210
FT SEQUENCE 210 AA; 21967 MW; 83782D98B6863C8 CRC64;
SQ
Query Match 8.3%; Score 151.5; DB 1; Length 210;
Best Local Similarity 26.9%; Pred. No. 0.0012;
Matches 52; Conservative 20; Mismatches 88; Indels 33; Gaps 9;
QY 11 AVALALSSAEAAAS--CSSVYQCQGIGWSGPTCCSGSTCVAGENKYYSOC--LPGSHS 67
Db 8 AAALTLSSAAAAAASACGVLYEQCGIGFDGVTCCSEGLMCMKM--GPYYSQCRAMPGMWG 65
QY 68 -----NNAGNASSTKTSTKTSTTTAKATAITTKTITTKTTTGTSTAASSTSS 122
Db 66 QVKPYQCQGGMYSKTWCSPGFCKVELNEFFSOCDLANKSPVATPKVSFTSPPGPAQVC 125
QY 123 SAGYKVISGKGSGSTTRYWDCK-----ASCWPFGRKASVTPGDTCASNGISLLDA 175
Db 126 GREY-AACGGEFMGA----KCKFGVLVCVETSGKWQSQRAPP-----KMGEV 170
QY 176 NAOQGCNGGNGFM 188
Db 171 GRYAQC-GMGYM 182
RESULT 12
MUCL_XENLA
ID MUCL_XENLA STANDARD; PRT; 662 AA.
AC Q05049;
AD 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Integratory mucin C.1 (FIM-C.1) (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6 AND 7).
RC TISSUE=Skin.
RX MEDLINE=93077556; PubMed=1447205;
RA Hauser F., Hoffmann W.;
RT "P-domains as shuffled cysteine-rich modules in integratory mucin
RT C.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic
RL polymorphism."
RL J. Biol. Chem. 267:24620-24624(1992).
CC 1- FUNCTION: COULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL
CC INFECTIIONS. PROTECTS THE EPITHELIA FROM EXTERNAL ENVIRONMENT.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- ALTERNATIVE PRODUCTS: At least 7 isoforms; 1 (shown here), 2, 3,
CC 4, 5, 6 and 7; may be produced by alternative splicing.
CC 1- TISSUE SPECIFICITY: SKIN.
CC 1- PTM: EXTENSIVELY O-GLYCOSYLATED.
CC 1- SIMILARITY: CONTAINS 6 P-TYPE (TREFOIL) DOMAINS.
CC
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OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RN RN